

SEQUENCE LISTING

<110> Munger, Karl and Syken, Josh

<120> Methods and Reagents to Regulate Apoptosis

<130> HMV-054.01

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<170> PatentIn version 3.0

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Thr Lys His Asn Pro Phe Ile Cys Thr Ala Ser Phe His Thr Ser Ala

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35 40 45
Ala Ser Ser Leu Thr Ser Cys Gly Pro Arg Ala Leu Leu Thr Leu Arg
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Pro Gly Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr
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Ala Ser Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln
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Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala
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Tyr Tyr Gln Leu Ala Lys Lys Tyr His Pro Asp Thr Asn Lys Asp Asp
115 120 125
Pro Lys Ala Lys Glu Lys Phe Ser Gln Leu Ala Glu Ala Tyr Glu Val
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Leu Ser Asp Glu Val Lys Arg Lys Gln Tyr Asp Ala Tyr Gly Ser Ala
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Gly Phe Asp Pro Gly Ala Ser Gly Ser Gln His Ser Tyr Trp Lys Gly
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260 265 270

Ser Thr Cys Arg Arg Cys Gly Gly Arg Gly Ser Ile Ile Ile Ser Pro
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Cys Val Val Cys Arg Gly Ala Gly Gln Ala Lys Gln Lys Lys Arg Val
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325 330 335

Pro Val Phe Arg Arg Asp Gly Ala Asp Ile His Ser Asp Leu Phe Ile
340 345 350

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355 360 365

Tyr Glu Thr Ile Asn Val Thr Ile Pro Pro Gly Thr Gln Thr Asp Gln
370 375 380

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385 390 395 400

Tyr Gly Asp His Tyr Ile His Ile Lys Ile Arg Val Pro Lys Arg Leu
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Thr Ser Arg Gln Gln Ser Leu Ile Leu Ser Tyr Ala Glu Asp Glu Thr
420 425 430

Asp Val Glu Gly Thr Val Asn Gly Val Thr Leu Thr Ser Ser Gly Gly
435 440 445

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: mRNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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GGC GTG GTG GGG GCA TGG CTG AGC CGC AAG CTG AGC GTC CCC GCC TTT	144
Gly Val Val Gly Ala Trp Leu Ser Arg Lys Leu Ser Val Pro Ala Phe	
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GCG TCT TCC CTG ACC TCT TGC GGC CCC CGA GCG CTG CTG ACA TTG AGA	192
Ala Ser Ser Leu Thr Ser Cys Gly Pro Arg Ala Leu Leu Thr Leu Arg	
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CCT GGT GTC AGC CTT ACA GGA ACA AAA CAT AAC CCT TTC ATT TGT ACT	240
Pro Gly Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr	
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GCC TCC TTC CAC ACG AGT GCC CCT TTG GCC AAA GAA GAT TAT TAT CAG	288
Ala Ser Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln	
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ATA TTA GGA GTG CCT CGA AAT GCC AGC CAG AAA GAG ATC AAG AAA GCC	336
Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala	
100 105 110	
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Gly	Phe	Asp	Pro	Gly	Ala	Ser	Gly	Ser	Gln	His	Ser	Tyr	Trp	Lys	Gly	
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Asn	Lys	Glu	Phe	Thr	Val	Asn	Ile	Met	Asp	Thr	Cys	Glu	Arg	Cys	Asn	
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Cys	Val	Val	Cys	Arg	Gly	Ala	Gly	Gln	Ala	Lys	Gln	Lys	Lys	Arg	Val	
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Pro	Val	Phe	Arg	Arg	Asp	Gly	Ala	Asp	Ile	His	Ser	Asp	Leu	Phe	Ile	
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Asp	Val	Glu	Gly	Thr	Val	Asn	Gly	Val	Thr	Leu	Thr	Ser	Ser	Gly	Gly		
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GAG	GAC	GAG	GAG	GGA	TTC	CTT	TCC	AAA	CTT	AAG	AAA	ATG	TTT	ACC	TCA	1440	
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TGA																	

1443

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Ala	Ala	Arg	Cys	Ser	Thr	Arg	Trp	Leu	Leu	Val	Val	Val	Gly	Thr		
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Pro	Arg	Leu	Pro	Ala	Ile	Ser	Gly	Arg	Gly	Ala	Arg	Pro	Pro	Arg	Glu		
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Ile	Leu	Gly	Val	Pro	Arg	Asn	Ala	Ser	Gln	Lys	Glu	Ile	Lys	Lys	Ala		
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Tyr	Tyr	Gln	Leu	Ala	Lys	Lys	Tyr	His	Pro	Asp	Thr	Asn	Lys	Asp	Asp		
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Pro	Lys	Ala	Lys	Glu	Lys	Phe	Ser	Gln	Leu	Ala	Glu	Ala	Tyr	Glu	Val		
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Gly	Pro	Thr	Val	Asp	Pro	Glu	Glu	Leu	Phe	Arg	Lys	Ile	Phe	Gly	Glu	
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TTC	TCA	TCC	TCT	TCA	TTT	GGA	GAT	TTC	CAG	ACC	GTG	TTT	GAT	CAG	CCT	624
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			195					200						205		
CAG	GAA	TAC	TTC	ATG	GAG	TTG	ACA	TTC	AAT	CAA	GCT	GCA	AAG	GGG	GTC	672
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Asn	Lys	Glu	Phe	Thr	Val	Asn	Ile	Met	Asp	Thr	Cys	Glu	Arg	Cys	Asn	
					230						235				240	
GGC	AAG	GGG	AAC	GAG	CCC	GGC	ACC	AAG	GTG	CAG	CAT	TGC	CAC	TAC	TGT	768
Gly	Lys	Gly	Asn	Glu	Pro	Gly	Thr	Lys	Val	Gln	His	Cys	His	Tyr	Cys	
			245						250					255		
GGC	GGC	TCC	GGC	ATG	GAA	ACC	ATC	AAC	ACA	GGC	CCT	TTT	GTG	ATG	CGT	816
Gly	Gly	Ser	Gly	Met	Glu	Thr	Ile	Asn	Thr	Gly	Pro	Phe	Val	Met	Arg	
			260					265						270		
TCC	ACG	TGT	AGG	AGA	TGT	GGT	GGC	CGC	GGC	TCC	ATC	ATC	ATA	TCG	CCC	864
Ser	Thr	Cys	Arg	Arg	Cys	Gly	Gly	Arg	Gly	Ser	Ile	Ile	Ile	Ser	Pro	
			275					280						285		
TGT	GTG	GTC	TGC	AGG	GGA	GCA	GGA	CAA	GCC	AAG	CAG	AAA	AAG	CGA	GTG	912
Cys	Val	Val	Cys	Arg	Gly	Ala	Gly	Gln	Ala	Lys	Gln	Lys	Lys	Arg	Val	
			290					295						300		
ATG	ATC	CCT	GTG	CCT	GCA	GGA	GTC	GAG	GAT	GGC	CAG	ACC	GTG	AGG	ATG	960
Met	Ile	Pro	Val	Pro	Ala	Gly	Val	Glu	Asp	Gly	Gln	Thr	Val	Arg	Met	
					310					315					320	
CCT	GTG	GGA	AAA	AGG	GAA	ATT	TTC	ATT	ACG	TTC	AGG	GTG	CAG	AAA	AGC	1008
Pro	Val	Gly	Lys	Arg	Glu	Ile	Phe	Ile	Thr	Phe	Arg	Val	Gln	Lys	Ser	
			325							330				335		
CCT	GTG	TTC	CGG	AGG	GAC	GGC	GCA	GAC	ATC	CAC	TCC	GAC	CTC	TTT	ATT	1056
Pro	Val	Phe	Arg	Arg	Asp	Gly	Ala	Asp	Ile	His	Ser	Asp	Leu	Phe	Ile	
			340					345						350		
TCT	ATA	GCT	CAG	GCT	CTT	CTT	GGG	GGA	ACA	GCC	AGA	GCC	CAG	GGC	CTG	1104
Ser	Ile	Ala	Gln	Ala	Leu	Leu	Gly	Gly	Thr	Ala	Arg	Ala	Gln	Gly	Leu	
			355					360						365		
TAC	GAG	ACG	ATC	AAC	GTG	ACG	ATC	CCC	CCT	GGG	ACT	CAG	ACA	GAC	CAG	1152
Tyr	Glu	Thr	Ile	Asn	Val	Thr	Ile	Pro	Pro	Gly	Thr	Gln	Thr	Asp	Gln	
			370				375					380				
AAG	ATT	CGG	ATG	GGT	GGG	AAA	GGC	ATC	CCC	CGG	ATT	AAC	AGC	TAC	GGC	1200
Lys	Ile	Arg	Met	Gly	Gly	Lys	Gly	Ile	Pro	Arg	Ile	Asn	Ser	Tyr	Gly	
					390					395					400	
TAC	GGA	GAC	CAC	TAC	ATC	CAC	ATC	AAG	ATA	CGA	GTT	CCA	AAG	AGG	CTA	1248
Tyr	Gly	Asp	His	Tyr	Ile	His	Ile	Lys	Ile	Arg	Val	Pro	Lys	Arg	Leu	
			405						410					415		
ACG	AGC	CGG	CAG	CAG	AGC	CTG	ATC	CTG	AGC	TAC	GCC	GAG	GAC	GAG	ACA	1296

Thr	Ser	Arg	Gln	Gln	Ser	Leu	Ile	Leu	Ser	Tyr	Ala	Glu	Asp	Glu	Thr		
			420					425					430				
GAT	GTG	GAG	GGG	ACG	GTG	AAC	GGC	GTC	ACC	CTC	ACC	AGC	TCT	GGA	AAA		1344
Asp	Val	Glu	Gly	Thr	Val	Asn	Gly	Val	Thr	Leu	Thr	Ser	Ser	Gly	Lys		
		435					440					445					
AGA	TCC	ACT	GGA	AAC	TAG												1362
Arg	Ser	Thr	Gly	Asn													
		450															

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Ala	Ala	Arg	Cys	Ser	Thr	Arg	Trp	Leu	Leu	Val	Val	Val	Gly	Thr		
1				5				10						15			
Pro	Arg	Leu	Pro	Ala	Ile	Ser	Gly	Arg	Gly	Ala	Arg	Pro	Pro	Arg	Glu		
			20					25					30				
Gly	Val	Val	Gly	Ala	Trp	Leu	Ser	Arg	Lys	Leu	Ser	Val	Pro	Ala	Phe		
		35					40					45					
Ala	Ser	Ser	Leu	Thr	Ser	Cys	Gly	Pro	Arg	Ala	Leu	Leu	Thr	Leu	Arg		
	50					55					60						
Pro	Gly	Val	Ser	Leu	Thr	Gly	Thr	Lys	His	Asn	Pro	Phe	Ile	Cys	Thr		
65				70				75						80			
Ala	Ser	Phe	His	Thr	Ser	Ala	Pro	Leu	Ala	Lys	Glu	Asp	Tyr	Tyr	Gln		
			85					90					95				
Ile	Leu	Gly	Val	Pro	Arg	Asn	Ala	Ser	Gln	Lys	Glu	Ile	Lys	Lys	Ala		
		100					105						110				
Tyr	Tyr	Gln	Leu	Ala	Lys	Lys	Tyr	His	Pro	Asp	Thr	Asn	Lys	Asp	Asp		
	115						120					125					
Pro	Lys	Ala	Lys	Glu	Lys	Phe	Ser	Gln	Leu	Ala	Glu	Ala	Tyr	Glu	Val		
	130					135					140						
Leu	Ser	Asp	Glu	Val	Lys	Arg	Lys	Gln	Tyr	Asp	Ala	Tyr	Gly	Ser	Ala		
145				150				155						160			
Gly	Phe	Asp	Pro	Gly	Ala	Ser	Gly	Ser	Gln	His	Ser	Tyr	Trp	Lys	Gly		
			165					170						175			
Gly	Pro	Thr	Val	Asp	Pro	Glu	Glu	Leu	Phe	Arg	Lys	Ile	Phe	Gly	Glu		
		180						185					190				
Phe	Ser	Ser	Ser	Ser	Phe	Gly	Asp	Phe	Gln	Thr	Val	Phe	Asp	Gln	Pro		
	195					200						205					
Gln	Glu	Tyr	Phe	Met	Glu	Leu	Thr	Phe	Asn	Gln	Ala	Ala	Lys	Gly	Val		
	210					215					220						
Asn	Lys	Glu	Phe	Thr	Val	Asn	Ile	Met	Asp	Thr	Cys	Glu	Arg	Cys	Asn		
225				230				235						240			
Gly	Lys	Gly	Asn	Glu	Pro	Gly	Thr	Lys	Val	Gln	His	Cys	His	Tyr	Cys		
			245					250						255			
Gly	Gly	Ser	Gly	Met	Glu	Thr	Ile	Asn	Thr	Gly	Pro	Phe	Val	Met	Arg		
		260					265						270				
Ser	Thr	Cys	Arg	Arg	Cys	Gly	Gly	Arg	Gly	Ser	Ile	Ile	Ile	Ser	Pro		
	275					280						285					
Cys	Val	Val	Cys	Arg	Gly	Ala	Gly	Gln	Ala	Lys	Gln	Lys	Lys	Arg	Val		
	290					295					300						
Met	Ile	Pro	Val	Pro	Ala	Gly	Val	Glu	Asp	Gly	Gln	Thr	Val	Arg	Met		
305				310				315						320			
Pro	Val	Gly	Lys	Arg	Glu	Ile	Phe	Ile	Thr	Phe	Arg	Val	Gln	Lys	Ser		

